

US-09-316-163-9.rpr

Fri Jun 9 10:53:46 2000

WIREH

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Thu Jun 8 21:37:37 2000: Maspar time 14.11 Seconds
692.177 Million cell updates/sec

Run on:
Tabular output not generated.
Title: >US-09-316-163-9
Description: (1-207) from US09316163.pap
Perfect Score: 1573
Sequence: 1 EDICNLPPTTITLIGWS.....VEISCKSPDVINGSPISOKI/207

Scoring table: PAM 150
Gap 11
Searched: 142080 seqs, 47172406 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r2
p1r1 2:p1r2 3:p1r3 4:p1r4
Mean 41.851; Variance 66.119; scale 0.633
Statistics: Mean 41.851; Variance 66.119; scale 0.633
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1573	100.0	449	1	complement factor H p	0.00e+00
2	1573	100.0	1231	1	complement factor H p	0.00e+00
3	1154	73.4	1234	1	factor H - bovine (fr	1.13e-265
4	679	43.2	669	2	probable complement r	6.86e-96
5	503	32.0	1053	2	C4BP alpha chain prec	6.02e-54
6	334	21.2	597	1	hypothetical protein	3.60e-48
7	310	19.7	560	2	E-selectin - pig	1.08e-47
8	308	19.6	830	2	p-selectin precursor	1.69e-46
9	308	19.6	830	2	apolipoprotein H homo	1.69e-46
10	303	19.3	768	2	p-selectin precursor	1.69e-46
11	303	19.3	768	2	p-selectin - rat	1.69e-46
12	297	18.9	245	1	apolipoprotein H prec	4.55e-45
13	297	18.9	245	1	endothelial leukocyte	2.63e-45
14	298	18.9	610	2	apolipoprotein H prec	7.01e-44
15	298	18.9	610	2	apolipoprotein H prec	7.01e-44
16	292	18.6	345	1	decay-accelerating fa	4.06e-44
17	293	18.6	345	1	decay-accelerating fa	4.06e-44
18	293	18.6	440	2	endothelial leukocyte	2.09e-43
19	290	18.4	551	2	C4b-binding protein a	2.09e-43
20	288	18.3	597	1	secretory complement	6.22e-43
21	288	18.3	360	1	membrane-bound comple	6.22e-43
22	288	18.3	612	2	endothelial leukocyte	6.22e-43

endothelial leukocyte 1.07e-42
decay-accelerating fa 5.49e-42
complement control pr 1.63e-41
sperm CD46 - human (f 2.80e-41
membrane cofactor pro 2.80e-41
membrane cofactor pro 2.80e-41
membrane cofactor pro 2.80e-41
E-selectin precursor 8.29e-41
complement C3b recept 4.21e-40
coagulation factor C- 4.21e-40
membrane cofactor pro 3.66e-39
membrane cofactor pro 1.08e-38
apolipoprotein H prec 1.08e-38
C4b-binding protein a 1.08e-38
complement C3b/C4b re 5.42e-38
complement C3b/C4b re 5.42e-38
E-selectin - bovine 9.28e-38
complement regulatory 2.72e-37
apolipoprotein H prec 2.72e-37
C4b-binding protein a 1.59e-37

ALIGNMENTS

RESULT 1
ENTRY NBHUS #type complete
TITLE complement factor H precursor, short splice form - human H
ALTERNATE_NAMES complement factor H-related protein; complement protein
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1993 #sequence_revision 23-Feb-1996 #text_change
31-Dec-1993
ACCESSIONS S03013; B60238; A27877; A61103; A26505; S10479
REFERENCE S03013
AUTHORS Ripoche, J.; Day, A.-J.; Harris, T.J.R.; Sim, R.B.
#journal The complete amino acid sequence of human complement factor H.
#title
#cross-references PMID:88134059
#molecule_type mRNA
#accession S03013
#residues 1-449 #label RIP
#cross-references EMBL:X00716; NID:932492;
PDB:CAA30403.1; PID:9758073
part of this sequence, including the amino end of the
mature protein was confirmed by protein sequencing
402-Tyr was also found
#note
#note A60238
REFERENCE A60238
AUTHORS Estaller, C.; Schwaebble, W.; Dierich, M.; Weiss, E.H.
#journal Eur. J. Immunol. (1991) 21:799-802
#title Human complement factor H: two factor H proteins are derived from alternatively spliced transcripts.
#cross-references MIM:1184292
#accession B60238
#status not compared with conceptual translation
#molecule_type mRNA
#residues 1-33,434-449 #label EST
#note only portions of this 1.8 kilobase mRNA were sequenced
#note A27877
REFERENCE A27877
AUTHORS Schulz, T.F.; Schwaebble, W.; Stanley, K.K.; Weiss, E.; Dierich, M.P.
#journal Eur. J. Immunol. (1986) 16:1351-1355
#title Human complement factor H: isolation of cDNA clones and partial cDNA sequence of the 38-kDa tryptic fragment containing the binding site for C3b.
#cross-references MIM:87054207
#accession A27877
#molecule_type mRNA
#residues '11', 55-401, '1', 403-449 #label SCH
#note an additional nucleotide present within the codon for Glu-310 was thought to be a cloning artifact and was ignored in translation

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#domain complement factor H repeat homology #label FH02\
#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH04\
#region cell attachment (R-G-D) motif\
#domain complement factor H repeat homology #label PH05\
#domain complement factor H repeat homology #label PH06\
#domain complement factor H repeat homology #label PH07\
85-141      *domain complement factor H repeat homology #label FH02\
146-205     *domain complement factor H repeat homology #label FH03\
210-262     *domain complement factor H repeat homology #label FH04\
246-248     *region cell attachment (R-G-D) motif\
267-320     *domain complement factor H repeat homology #label PH05\
325-385     *domain complement factor H repeat homology #label PH06\
389-442     *domain complement factor H repeat homology #label PH07\
21-66,52-80,85-129,
114-141,146-192,
178-205,210-251,
237-262,267-309,
294-320,325-374,
357-385,389-431,
416-442
217
SUMMARY
length 449 #molecular-weight 51007 #checksum 6077
disulfide_bonds #status predicted\
binding_site carbohydrate (Asn) (covalent) #status absent
Query Match          100.0%   Score 1573; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.00e+00; Gaps 0;
Matches              207; Conservative
Db                  19 EDCNELPPRRNTTEILTGSDQTYPEQTGTAIKCPGYSLGNVIMVKRGKGEVALNPLR 60
QY                   1 EDCNELPPRRNTTEILTGSDQTYPEGTGTAIKCPGYSLGNVIMVKRGKGEVALNPLR 138
Db                    79 KCKRPCCGHDPDFTFLLTGGNVFEYGKVAYTCNGEYQLLGEINRYRECDTDGWNTDI 120
QY                     61 KCKRPCCGHDPDFTFLLTGGNVFEYGKVAYTCNGEYQLLGEINRYRECDTDGWNTDI 198
Db                      139 PICEVVKKLPVTAPENKIVSSAMEPDREVHFGQAVRFVCNSGYKIEDEMHCSDDGFW 180
QY                       121 PICEVVKKLPVTAPENKIVSSAMEPDREVHFGQAVRFVCNSGYKIEDEMHCSDDGFW 180
Db                        199 SKPKPCVEISCKSPDVINGSPISKI 225
QY                         181 SKPKPCVEISCKSPDVINGSPISKI 207
RESULT                2
ENTRY                 NBHUH           #type complete
TITLE                 Complement factor H precursor, long splice form - human
ORGANISM              Homo sapiens    #common_name man
DATE                  31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
ACCESSIONS            S00254; A60238; A54726; A61565; A26505; I72654; S66298
REFERENCE              Ripoché, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B.
                     Biochem. J. (1988) 249:593-602.
                     The complete amino acid sequence of human complement factor H.
cross-references MUID:88134059
accession             S00254
molecule_type        mRNA
residues              1-1231 #label RIP
note                  402-Tyr was also found
cross-references EMBL:I00716; NID:g31964; PIDN:CAG68704.1; PID:g31965
note                  parts of this sequence, including the amino and carboxyl ends of the mature protein, were confirmed by protein sequencing
A60238               Escallier, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H.
author               Eur. J. Immunol. (1991) 21:799-802
journal              Human complement factor H: two factors are derived from alternatively spliced transcripts.
title                cross-references MUID:9184292
accession            A60238
status               not compared with conceptual translation
molecule_type       mRNA
residues             1-56;1177-1231 #label EST
note                 only portions of this 4.3 kilobase mRNA were sequenced
reference            A54726
author               Day, A.J.; Ripoché, J.; Lyons, A.; McIntosh, B.; Harris,
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